

PAGE: 1

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/403,262DATE: 04/20/2000
TIME: 00:36:00

INPUT SET: S35332.raw

This Raw Listing contains the General
Information Section and those Sequences
containing ERRORS.

Does Not Comply
Corrected Diskette Needed

SEQUENCE LISTING

(1) General Information:

(i) APPLICANT: *move up - all responses must be on same line or leading*
~~(A) NAME: Nikolaus (Klaus) Theres~~
~~(B) STREET: Schiffgesweg 30~~
~~(C) CITY: Pulheim~~
~~(D) STATE: NRW~~
~~(E) COUNTRY: Germany~~
~~(F) POSTAL CODE: 50259~~
~~(G) TELEPHONE: + 49 2234 89386~~

(ii) TITLE OF INVENTION: PLANTS WITH CONTROLLED SIDE SHOOTFORMATION AND/OR ABSC?

(iii) NUMBER OF SEQUENCES: 14

*add these mandatory headings**all text must
be visible*

(iv) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC DOS/MS DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPA)

*and responses
for a U.S. case*

Correspondence Address:
(A) ADDRESSEE:
(B) STREET:
(C) CITY:
(D) STATE:
(E) COUNTRY:
(F) ZIP:

NO CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

add these headings for a U.S. case

ERRORED SEQUENCES FOLLOW:

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 428 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Lycopersicon esculentum*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

1) EPO format of
PatentIn is
invalid for a U.S.
case.

2) See item 5 on
Erra Summary sheet.

3) All U.S. cases filed

Publ: on or after July 1, 1998,
which cannot claim a
prior U.S. case or a prior
international case
designating the United States,
needs to be in new Sequence Rules
format.

*add
opening
parenthesis*

RAW SEQUENCE LISTING PATENT APPLICATION US/09/403,262

DATE: 04/20/2000
TIME: 00:36:00

INPUT SET: S35332.raw

```

116
--> 117 Met Leu Gly Ser Phe Gly Ser Ser Ser Ser Gln Ser His Pro HisHis
118 1 5 10 15
119
--> 120 Asp Glu Glu Ser Ser Asp His His Gln Gln Arg Arg Phe Thr AlaThr
121 20 25 30
122
--> 123 Ala Thr Thr Ile Thr Thr Thr Thr Ile Thr Thr Ser Pro Ala IleGln
124 35 40 45
--> 125 Ile Arg Gln Leu Leu Ile Ser Cys Ala Glu Leu Ile Ser Gln SerAsp
126 50 55 60
127
--> 128 Phe Ser Ala Ala Lys Arg Leu Leu Thr Ile Leu Ser Thr Asn SerSer
129 65 70 75 80
130
--> 131 Pro Phe Gly Asp Ser Thr Glu Arg Leu Val His Gln Phe Thr ArgAla
132 85 90 95
133
--> 134 Leu Ser Leu Arg Leu Asn Arg Tyr Ile Ser Ser Thr Thr Asn HisPhe
135 100 105 110
136
--> 137 Met Thr Pro Val Glu Thr Thr Pro Thr Asp Ser Ser Ser SerSer
138 115 120 125
139
--> 140 Leu Ala Leu Ile Gln Ser Ser Tyr Leu Ser Leu Asn Gln Val ThrPro
141 130 135 140
142
--> 143 Phe Ile Arg Phe Thr Gln Leu Thr Ala Asn Gln Ala Ile Leu GluAla
144 145 150 155 160
145
--> 146 Ile Asn Gly Asn His Gln Ala Ile His Ile Val Asp Phe Asp IleAsn
147 165 170 175
148
--> 149 His Gly Val Gln Trp Pro Pro Leu Met Gln Ala Leu Ala Asp ArgTyr
150 180 185 190
151
--> 152 Pro Ala Pro Thr Leu Arg Ile Thr Gly Thr Gly Asn Asp Leu AspThr
153 195 200 205
154
--> 155 Leu Arg Arg Thr Gly Asp Arg Leu Ala Lys Phe Ala His Ser LeuGly
156 210 215 220
--> 157 Leu Arg Phe Gln Phe His Pro Leu Tyr Ile Ala Asn Asn Asn HisAsp
158 225 230 235 240
159
--> 160 His Asp Glu Asp Pro Ser Ile Ile Ser Ser Ile Val Leu Leu ProAsp
161 245 250 255
162
--> 163 Glu Thr Leu Ala Ile Asn Cys Val Phe Tyr Leu His Arg Leu LeuLys
164 260 265 270
165
--> 166 Asp Arg Glu Lys Leu Arg Ile Phe Leu His Arg Val Lys Ser MetAsn
167 275 280 285
168

```

insert a
space
between
amino
acids.
Do NOT
use TAB
codes
between
amino
acids.
Use
space
characters.

fix
numbers

RAW SEQUENCE LISTING PATENT APPLICATION US/09/403,262

DATE: 04/20/2000
TIME: 00:36:01

INPUT SET: S35332.raw

```

--> 382   Ile Arg Gln Leu Leu Ile Ser Cys Ala Glu Leu Ile Ser Arg SerAsp
      383         50             55             60
      384
--> 385   Phe Ser Ala Ala Lys Arg Leu Leu Thr Ile Leu Ser Thr Asn SerSer
      386         65             70             75             80
      387
--> 388   Pro Phe Gly Asp Ser Thr Glu Arg Leu Val His Gln Phe Thr ArgAla
      389             85             90             95
      390
--> 391   Leu Ser Leu Arg Leu Asn Arg Tyr Ile Ser Ser Thr Thr Asn HisPhe
      392             100             105             110
      393
--> 394   Met Thr Pro Val Glu Thr Thr Pro Thr Asp Ser Ser Ser Ser LeuPro
      395             115             120             125
      396
--> 397   Ser Ser Ser Leu Ala Leu Ile Gln Ser Ser Tyr His Ser Leu AsnGln
      398             130             135             140
      399
--> 400   Val Thr Pro Phe Ile Arg Phe Thr Gln Leu Thr Ala Asn Gln AlaIle
      401             145             150             155             160
      402
--> 403   Leu Glu Ala Ile Asn Gly Asn His Gln Ala Ile His Ile Val AspPhe
      404             165             170             175
      405
--> 406   Asp Ile Asn His Gly Val Gln Trp Pro Pro Leu Met Gln Ala LeuAla
      407             180             185             190
      408
--> 409   Asp Arg Tyr Pro Ala Pro Thr Leu Arg Ile Thr Gly Thr Gly AsnAsp
      410             195             200             205
      411
--> 412   Leu Asp Thr Leu Arg Arg Thr Gly Asp Arg Leu Ala Lys Phe AlaHis
      413             210             215             220
      414
--> 415   Ser Leu Gly Leu Arg Phe Gln Phe His Pro Leu Tyr Ile Ala AsnAsn
      416             225             230             235             240
      417
--> 418   Asn Arg Asp His Gly Glu Asp Pro Ser Ile Ile Ser Ser Ile ValLeu
      419             245             250             255
      420
--> 421   Leu Pro Asp Glu Thr Leu Ala Ile Asn Cys Val Phe Tyr Leu HisArg
      422             260             265             270
      423
--> 424   Leu Leu Lys Asp Arg Glu Lys Leu Arg Ile Phe Leu His Arg Vallys
      425             275             280             285
      426
--> 427   Ser Met Asn Pro Lys Ile Val Thr Ile Ala Glu Lys Glu Ala AsnHis
      428             290             295             300
      429
--> 430   Asn His Pro Leu Phe Leu Gln Arg Phe Ile Glu Ala Leu Asp TyrTyr
      431             305             310             315             320
      432
--> 433   Thr Ala Val Phe Asp Ser Leu Glu Ala Thr Leu Pro Pro Gly SerArg
      434             325             330             335

```

Insert
 a space
 between
 last
 two
 amino
 acids on
 each
 line

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/403,262DATE: 04/20/2000
TIME: 00:36:01

INPUT SET: S35332.raw

```
435
--> 436   Glu Arg Met Thr Val Glu Gln Val Trp Phe Gly Arg Glu Ile ValAsp
437           340           345           350
--> 438   Ile Val Ala Met Glu Gly Asp Lys Arg Lys Glu Arg His Glu ArgPhe
439           355           360           365
440
--> 441   Arg Ser Trp Glu Val Met Leu Arg Ser Cys Gly Phe Ser Asn ValAla
442           370           375           380
443
--> 444   Leu Ser Pro Phe Ala Leu Ser Gln Ala Lys Leu Leu Leu Arg LeuHis
445           385           390           395           400
446
--> 447   Tyr Pro Ser Glu Gly Tyr Gln Leu Gly Val Ser Ser Asn Ser PhePhe
448           405           410           415
449
450   Leu Gly Trp Gln Asn Gln Pro Leu Phe Ser Ile Ser Ser Trp Arg
451           420           425           430
452
453
```

```
531   (2) INFORMATION FOR SEQ ID NO: 14:
532
533   (i) SEQUENCE CHARACTERISTICS:
--> 534       (A) LENGTH: 229 amino acids
535       (B) TYPE: amino acid
536       (C) STRANDEDNESS: single
537       (D) TOPOLOGY: linear
538
539   (ii) MOLECULE TYPE: Protein
540
541   (vi) ORIGINAL SOURCE:
542       (A) ORGANISM: Arabidopsis thaliana
543
544   (xi) SEQUENCE DESCRIPTION: SE
```

please ignore blank section!

Agave blank section

same
error
as previous
pages

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/403,262DATE: 04/20/2000
TIME: 00:36:02

INPUT SET: S35332.raw

--> 564 Phe Leu Ser Ala Ile Lys Ser Leu Asn Ser Arg Ile Val Thr MetAla
565 100 105 110
566
--> 567 Glu Arg Glu Ala Asn His Gly Asp His Ser Phe Leu Asn Arg PheSer
568 115 120 125
569
--> 570 Glu Ala Val Asp His Tyr Met Ala Ile Phe Asp Ser Leu Glu AlaThr
571 130 135 140
572
--> 573 Leu Pro Pro Asn Ser Arg Glu Arg Leu Thr Leu Glu Gln Arg TrpPhe
574 145 150 155 160
575
--> 576 Gly Lys Glu Ile Leu Asp Val Val Ala Ala Glu Glu Thr Glu ArgLys
577 165 170 175
578
--> 579 Gln Arg His Arg Arg Phe Glu Ile Trp Glu Glu Met Met Lys ArgPhe
580 180 185 190
581
--> 582 Gly Phe Val Asn Val Pro Ile Gly Ser Phe Ala Leu Ser Gln AlaLys
583 195 200 205
584
--> 585 Leu Leu Leu Arg Leu His Tyr Pro Ser Glu Gly Tyr Asn Leu GlnPhe
586 210 215 220
587
588 Leu Asn Asn Ser Leu
589 225
590
591

same

SEQUENCE VERIFICATION REPORT

PATENT APPLICATION US/09/403,262

DATE: 04/20/2000
TIME: 00:36:02

INPUT SET: S35332.raw

Line	Error	Original Text
5	Mandatory Value Not Present	(i) APPLICANT:
6	Unknown or Misplaced Identifier	(A) NAME: Nikolaus (Klaus) Theres
7	Unknown or Misplaced Identifier	(B) STREET: Schiffgesweg 30
8	Unknown or Misplaced Identifier	(C) CITY: Pulheim
9	Unknown or Misplaced Identifier	(D) STATE: NRW
10	Unknown or Misplaced Identifier	(E) COUNTRY: Germany
11	Unknown or Misplaced Identifier	(F) POSTAL CODE: 50259
12	Unknown or Misplaced Identifier	(G) TELEPHONE: + 49 2234 89386
105	Entered (428) and Calc. Seq. Length (376) differ	(A) LENGTH: 428 amino acids
113	Unknown or Misplaced Identifier	(A) ORGANISM: Lycopersicon esculentum
117	Wrong Amino Acid Designator	Met Leu Gly Ser Phe Gly Ser Ser Ser Ser Gln Ser His Pro H
120	Wrong Amino Acid Designator	Asp Glu Glu Ser Ser Asp His His Gln Gln Arg Arg Phe Thr
123	Wrong Amino Acid Designator	Ala Thr Thr Ile Thr Thr Thr Thr Ile Thr Thr Ser Pro Ala Ile
125	Wrong Amino Acid Designator	Ile Arg Gln Leu Leu Ile Ser Cys Ala Glu Leu Ile Ser Gln Se
128	Wrong Amino Acid Designator	Phe Ser Ala Ala Lys Arg Leu Leu Thr Ile Leu Ser Thr Asn
131	Wrong Amino Acid Designator	Pro Phe Gly Asp Ser Thr Glu Arg Leu Val His Gln Phe Thr
134	Wrong Amino Acid Designator	Leu Ser Leu Arg Leu Asn Arg Tyr Ile Ser Ser Thr Thr Asn
137	Wrong Amino Acid Designator	Met Thr Pro Val Glu Thr Thr Pro Thr Asp Ser Ser Ser Ser S
140	Wrong Amino Acid Designator	Leu Ala Leu Ile Gln Ser Ser Tyr Leu Ser Leu Asn Gln Val T
143	Wrong Amino Acid Designator	Phe Ile Arg Phe Thr Gln Leu Thr Ala Asn Gln Ala Ile Leu G
146	Wrong Amino Acid Designator	Ile Asn Gly Asn His Gln Ala Ile His Ile Val Asp Phe Asp Il
149	Wrong Amino Acid Designator	His Gly Val Gln Trp Pro Pro Leu Met Gln Ala Leu Ala Asp
152	Wrong Amino Acid Designator	Pro Ala Pro Thr Leu Arg Ile Thr Gly Thr Gly Asn Asp Leu
155	Wrong Amino Acid Designator	Leu Arg Arg Thr Gly Asp Arg Leu Ala Lys Phe Ala His Se
157	Wrong Amino Acid Designator	Leu Arg Phe Gln Phe His Pro Leu Tyr Ile Ala Asn Asn Asn
160	Wrong Amino Acid Designator	His Asp Glu Asp Pro Ser Ile Ile Ser Ser Ile Val Leu Leu Pro
163	Wrong Amino Acid Designator	Glu Thr Leu Ala Ile Asn Cys Val Phe Tyr Leu His Arg Leu
166	Wrong Amino Acid Designator	Asp Arg Glu Lys Leu Arg Ile Phe Leu His Arg Val Lys Ser
169	Wrong Amino Acid Designator	Pro Lys Ile Val Thr Ile Ala Glu Lys Glu Ala Asn His Asn H
172	Wrong Amino Acid Designator	Leu Phe Leu Gln Arg Phe Ile Glu Ala Leu Asp Tyr Tyr Thr
175	Wrong Amino Acid Designator	Phe Asp Ser Leu Glu Ala Thr Leu Pro Pro Gly Ser Arg Glu
178	Wrong Amino Acid Designator	Thr Val Glu Gln Val Trp Phe Gly Arg Glu Ile Val Asp Ile V
181	Wrong Amino Acid Designator	Met Glu Gly Asp Lys Arg Lys Glu Arg His Glu Arg Phe A
184	Wrong Amino Acid Designator	Glu Val Met Leu Arg Ser Cys Gly Phe Ser Asn Val Ala Leu
187	Wrong Amino Acid Designator	Phe Ala Leu Ser Gln Ala Lys Leu Leu Leu Arg Leu His Tyr
190	Wrong Amino Acid Designator	Glu Gly Tyr Gln Leu Gly Val Ser Ser Asn Ser Phe Phe Leu
361	Entered (431) and Calc. Seq. Length (379) differ	(A) LENGTH: 431 amino acids
373	Wrong Amino Acid Designator	Met Leu Gly Ser Phe Gly Ser Ser Ser Ser Gln Ser His Pro H
376	Wrong Amino Acid Designator	Asp Glu Glu Ser Ser Asp His His Gln Arg Arg Phe Thr
379	Wrong Amino Acid Designator	Thr Thr Thr Ile Thr Thr Thr Thr Thr Thr Thr Ser Pro Ala I
382	Wrong Amino Acid Designator	Ile Arg Gln Leu Leu Ile Ser Cys Ala Glu Leu Ile Ser Arg Se
385	Wrong Amino Acid Designator	Phe Ser Ala Ala Lys Arg Leu Leu Thr Ile Leu Ser Thr Asn
388	Wrong Amino Acid Designator	Pro Phe Gly Asp Ser Thr Glu Arg Leu Val His Gln Phe Thr
391	Wrong Amino Acid Designator	Leu Ser Leu Arg Leu Asn Arg Tyr Ile Ser Ser Thr Thr Asn
394	Wrong Amino Acid Designator	Met Thr Pro Val Glu Thr Thr Pro Thr Asp Ser Ser Ser Ser L
397	Wrong Amino Acid Designator	Ser Ser Ser Leu Ala Leu Ile Gln Ser Ser Tyr His Ser Leu As
400	Wrong Amino Acid Designator	Val Thr Pro Phe Ile Arg Phe Thr Gln Leu Thr Ala Asn Gln
403	Wrong Amino Acid Designator	Leu Glu Ala Ile Asn Gly Asn His Gln Ala Ile His Ile Val As

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/09/403,262DATE: 04/20/2000
TIME: 00:36:02

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Line	Error	Original Text
406	Wrong Amino Acid Designator	Asp Ile Asn His Gly Val Gln Trp Pro Pro Leu Met Gln Ala
409	Wrong Amino Acid Designator	Asp Arg Tyr Pro Ala Pro Thr Leu Arg Ile Thr Gly Thr Gly
412	Wrong Amino Acid Designator	Leu Asp Thr Leu Arg Arg Thr Gly Asp Arg Leu Ala Lys Ph
415	Wrong Amino Acid Designator	Ser Leu Gly Leu Arg Phe Gln Phe His Pro Leu Tyr Ile Ala
418	Wrong Amino Acid Designator	Asn Arg Asp His Gly Glu Asp Pro Ser Ile Ile Ser Ser Ile Va
421	Wrong Amino Acid Designator	Leu Pro Asp Glu Thr Leu Ala Ile Asn Cys Val Phe Tyr Leu
424	Wrong Amino Acid Designator	Leu Leu Lys Asp Arg Glu Lys Leu Arg Ile Phe Leu His Arg
427	Wrong Amino Acid Designator	Ser Met Asn Pro Lys Ile Val Thr Ile Ala Glu Lys Glu Ala A
430	Wrong Amino Acid Designator	Asn His Pro Leu Phe Leu Gln Arg Phe Ile Glu Ala Leu Asp
433	Wrong Amino Acid Designator	Thr Ala Val Phe Asp Ser Leu Glu Ala Thr Leu Pro Pro Gly
436	Wrong Amino Acid Designator	Glu Arg Met Thr Val Glu Gln Val Trp Phe Gly Arg Glu Ile
438	Wrong Amino Acid Designator	Ile Val Ala Met Glu Gly Asp Lys Arg Lys Glu Arg His Glu
441	Wrong Amino Acid Designator	Arg Ser Trp Glu Val Met Leu Arg Ser Cys Gly Phe Ser Asn
444	Wrong Amino Acid Designator	Leu Ser Pro Phe Ala Leu Ser Gln Ala Lys Leu Leu Leu Arg
447	Wrong Amino Acid Designator	Tyr Pro Ser Glu Gly Tyr Gln Leu Gly Val Ser Ser Asn Ser P
534	Entered (229) and Calc. Seq. Length (201) differ	(A) LENGTH: 229 amino acids
546	Wrong Amino Acid Designator	Glu Arg Ser Ser Asn Pro Ser Ser Pro Pro Pro Ser Leu Arg I
549	Wrong Amino Acid Designator	Gly Cys Gly Arg Asp Val Thr Gly Leu Asn Arg Thr Gly As
552	Wrong Amino Acid Designator	Thr Arg Phe Ala Asp Ser Leu Gly Leu Gln Phe Gln Phe His
555	Wrong Amino Acid Designator	Val Ile Val Glu Glu Asp Leu Ala Gly Leu Leu Leu Gln Ile A
558	Wrong Amino Acid Designator	Leu Ala Leu Ser Ala Val Gln Gly Glu Thr Ile Ala Val Asn C
561	Wrong Amino Acid Designator	His Phe Leu His Lys Ile Phe Asn Asp Asp Gly Asp Met Ile
564	Wrong Amino Acid Designator	Phe Leu Ser Ala Ile Lys Ser Leu Asn Ser Arg Ile Val Thr M
567	Wrong Amino Acid Designator	Glu Arg Glu Ala Asn His Gly Asp His Ser Phe Leu Asn Arg
570	Wrong Amino Acid Designator	Glu Ala Val Asp His Tyr Met Ala Ile Phe Asp Ser Leu Glu
573	Wrong Amino Acid Designator	Leu Pro Pro Asn Ser Arg Glu Arg Leu Thr Leu Glu Gln Ar
576	Wrong Amino Acid Designator	Gly Lys Glu Ile Leu Asp Val Val Ala Ala Glu Glu Thr Glu
579	Wrong Amino Acid Designator	Gln Arg His Arg Arg Phe Glu Ile Trp Glu Glu Met Met Lys
582	Wrong Amino Acid Designator	Gly Phe Val Asn Val Pro Ile Gly Ser Phe Ala Leu Ser Gln A
585	Wrong Amino Acid Designator	Leu Leu Leu Arg Leu His Tyr Pro Ser Glu Gly Tyr Asn Leu

PAGE: 1

SEQUENCE MISSING ITEM REPORT
PATENT APPLICATION US/09/403,262

DATE: 04/20/2000
TIME: 00:36:02

INPUT SET: S35332.raw

ADDRESSEE
STREET
CITY
STATE
COUNTRY
ZIP
CORRESPONDENCE ADDRESS
APPLICATION NUMBER
FILING DATE
CLASSIFICATION
CURRENT APPLICATION DATA
APPLICATION NUMBER
FILING DATE
PRIOR APPLICATION DATA